

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/549,997
Source: P4710
Date Processed by STIC: 10/3/05

ENTERED



PCT

RAW SEQUENCE LISTING

DATE: 10/03/2005

PATENT APPLICATION: US/10/549,997

TIME: 14:53:07

Input Set : A:\2107-283.ST25.txt

Output Set: N:\CRF4\10032005\J549997.raw

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3 <110> APPLICANT: Greiner, Steffen
4     Harms, Karsten
5     Kunz, Markward
6     Munir, Mohammad
7     Rausch, Thomas
8     Schirmer, Markus
10 <120> TITLE OF INVENTION: ALTERED PPASE IN SUGAR BEET
12 <130> FILE REFERENCE: P/2107-283
C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/549,997
C--> 15 <141> CURRENT FILING DATE: 2005-09-20
17 <150> PRIOR APPLICATION NUMBER: DE 103 13 795.5
18 <151> PRIOR FILING DATE: 2003-03-20
20 <160> NUMBER OF SEQ ID NOS: 21
22 <170> SOFTWARE: PatentIn version 3.3
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 1041
26 <212> TYPE: DNA
27 <213> ORGANISM: Beta vulgaris
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34 ggatgaggag atgaatgctg ttgcggagat gaatgctgtt gcttctaaag taaaagaaga      180
36 gtatcgccga gctccgaagt tgaaccaaag gatcatttcg tcaatgtcaa ggagatctgt      240
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40 tgttgttgag atacctaaag ggagcaaggt caagtatgag cttgacaaga aaactggact      360
42 tattatggtt gatcgaatat tatactcatc tgtggtctat cctcacaact atgggttttat      420
44 tccaagaaca ttgtgcgaag atggtgaccc catggatgtt ttagtgctca tgcaggaacc      480
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50 cactgatatc aaccagcttc ctccctcatcg tttggctgag atcagacgct tttttgagga      660
52 ctacaagaaa aatgagaaca aagaggttgc agtgaatgaa tttttgccag ctcaaattgc      720
54 tcatgatgcc atccagcact ctatggatct ctatgcggaa tacatcctac agacattgag      780
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60 tcccaaaaaga aagaaaagga gattttccct gttccttttc tgaatcttct tgtcgaaaat      960
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64 tcatgtttgg tttaggaggc t                                     1041
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69 <212> TYPE: PRT
70 <213> ORGANISM: Beta vulgaris
72 <400> SEQUENCE: 2
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75 1          5          10          15
78 Lys Val Lys Glu Glu Tyr Arg Arg Ala Pro Lys Leu Asn Gln Arg Ile
79          20          25          30
82 Ile Ser Ser Met Ser Arg Arg Ser Val Ala Ala His Pro Trp His Asp
83          35          40          45
86 Leu Glu Ile Gly Pro Asn Ala Pro Glu Ile Cys Asn Cys Val Val Glu
87          50          55          60
90 Ile Pro Lys Gly Ser Lys Val Lys Tyr Glu Leu Asp Lys Lys Thr Gly
91 65          70          75          80
94 Leu Ile Met Val Asp Arg Ile Leu Tyr Ser Ser Val Val Tyr Pro His
95          85          90          95
98 Asn Tyr Gly Phe Ile Pro Arg Thr Leu Cys Glu Asp Gly Asp Pro Met
99          100          105          110
102 Asp Val Leu Val Leu Met Gln Glu Pro Val Val Pro Gly Arg Phe Leu
103          115          120          125
106 Arg Ala Arg Ala Ile Gly Leu Met Pro Met Ile Asp Gln Gly Glu Lys
107          130          135          140
110 Asp Asp Lys Ile Ile Ala Val Cys Ala Asp Asp Pro Glu Val Arg His
111 145          150          155          160
114 Tyr Thr Asp Ile Asn Gln Leu Pro Pro His Arg Leu Ala Glu Ile Arg
115          165          170          175
118 Arg Phe Phe Glu Asp Tyr Lys Lys Asn Glu Asn Lys Glu Val Ala Val
119          180          185          190
122 Asn Glu Pro Leu Pro Ala Gln Ile Ala His Asp Ala Ile Gln His Ser
123          195          200          205
126 Met Asp Leu Tyr Ala Glu Tyr Ile Leu Gln Thr Leu Arg Arg
127          210          215          220
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131 <211> LENGTH: 245
132 <212> TYPE: PRT
133 <213> ORGANISM: Beta vulgaris
135 <400> SEQUENCE: 3
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142          20          25          30
145 Lys Glu Glu Tyr Arg Arg Ala Pro Lys Leu Asn Gln Arg Ile Ile Ser
146          35          40          45
149 Ser Met Ser Arg Arg Ser Val Ala Ala His Pro Trp His Asp Leu Glu
150          50          55          60
153 Ile Gly Pro Asn Ala Pro Glu Ile Cys Asn Cys Val Val Glu Ile Pro
154 65          70          75          80
157 Lys Gly Ser Lys Val Lys Tyr Glu Leu Asp Lys Lys Thr Gly Leu Ile
158          85          90          95
161 Met Val Asp Arg Ile Lys Tyr Ser Ser Val Val Tyr Pro His Asn Tyr
162          100          105          110
165 Gly Phe Ile Pro Arg Thr Leu Cys Glu Asp Gly Asp Pro Met Asp Val
166          115          120          125
169 Leu Val Leu Met Gln Glu Pro Val Val Pro Gly Arg Phe Leu Arg Ala

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170      130      135      140
173 Arg Ala Ile Gly Leu Met Pro Met Ile Asp Gln Gly Glu Leu Asp Asp
174 145      150      155      160
177 Lys Ile Ile Ala Val Cys Ala Asp Asp Pro Glu Val Arg His Tyr Thr
178      165      170      175
181 Asp Ile Asn Gln Leu Pro Pro His Arg Leu Ala Glu Ile Arg Arg Phe
182      180      185      190
185 Phe Glu Asp Tyr Lys Lys Asn Glu Asn Lys Glu Val Ala Val Asn Glu
186      195      200      205
189 Phe Leu Pro Ala Gln Ile Ala His Asp Ala Ile Gln His Ser Met Asp
190      210      215      220
193 Leu Tyr Ala Glu Tyr Ile Leu Gln Thr Leu Arg Arg Val Asp Leu Gln
194 225      230      235      240
197 Pro Ser Leu Ile Ser
198      245
201 <210> SEQ ID NO: 4
202 <211> LENGTH: 2810
203 <212> TYPE: DNA
204 <213> ORGANISM: Beta vulgaris
206 <400> SEQUENCE: 4
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211 agctcttctt ccagatctca taacagagat tatcattcct gtatgtgctg taattggaat 180
213 tgctttctct ctctttcaat ggtacatcgt ttctcaggtc aagctttccc ctgactctac 240
215 ccgcaataat aacaacaaaa atggattttc tgatagtttg attgaagaag aagaaggctc 300
217 taatgaccaa agtggtgttg ctaaatgtgc tgaaattcag aatgctattt ctgaaggggc 360
219 aacttccttc cttttcaccg agtaccagta tggttggtatc tttatgggtg cttttgctgt 420
221 gttgatattc cttttcctcg gatctgtgga gggtttcagc acaagtagcc aggaatgtac 480
223 ctatgacaaa accaggagggt gcaagcctgc tcttgccact gctatcttca gcacagtggc 540
225 cttcttgctt ggcgctatca cttctttggg ttctggtttc ttcgggatga agattgccac 600
227 atacgcaaat gcccgacaaa cactagaggc tagaaagggg gtcggcaaaag cattcattgt 660
229 agcattcagg tctggagctg tcatgggatt cctacttgct gcaaattggtc ttttggtgct 720
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233 ggctataact ggttatggtc ttggaggatc atccatggcc cttttcggtg gagttgctgg 840
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255 ctatttttgc cattgctatc agcattttcg tcagttttag ctttgcagct atgtatggta 1500
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259 atggccctat cagtgataat gctggaggca ttgctgagat ggctggtagt agccacagaa 1620
261 tccgtgagag aactgatgcc cttgatgctg ctggaaacac aaccgctgct attggaaagg 1680
263 gttttgcaat cggttctgca gctcttggtt ctcttgctct ctttggtgct tttgtaagcc 1740

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267 gagccatgct tccatactgg ttctctgccg tgacaatgaa gagtgtggga agtgcagctt 1860
269 tgaaaatggt tgaggaggtc cgaaggcaat tcaacaccat ccctggcttg ctggaaggca 1920
271 ctgccaaacc cgactatgct acctgtgtca agatctccac tgatgcttcc atcaaggaga 1980
273 tgatccccc aggtgctctt gtcattgtca caccattgat tgttggaaacc ttctttggtg 2040
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277 ctgcatccaa cactggtggt gcttgggaca atgccaagaa gtacattgag gctggtgctt 2160
279 cagagcatgc aaggacactt ggtcccaagg gatcagatgc acacaaggca gctgtgatcg 2220
281 gtgacaccat cggtgaccca cttaaggaca catcaggacc atcactcaac attctaata 2280
283 agcttatggc tgcagagtcg ctagtgttcg ccccttctt cgcacccac ggtggcttgc 2340
285 tcttcaagta cctctaaata tgatcggcgc aaaatcagaa ggcgacagag ggaggaattc 2400
287 gcggtttctt ctctcattt tgcgcctac aaatcgggca agttttaaat ttatcgcac 2460
289 aatttttgaa tgcgttaga tgacaactac aaggctggag gggctaaaac ttctacatga 2520
291 tgatgatgat aatgataatt tggaagcaag tcttgtgaaa aatagagtta tatggtcaac 2580
293 attattcttt tctttttctt tccttttatt gtaagatcgg gattttagt aatcattttg 2640
295 caaacctctt ttgttaggta taactcattt tctattttag tccttcagaa attgcatgca 2700
297 gttgcccttt tattttctaa aaagagaacc tgttcttgag catgtgttgt aagggcagaa 2760
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302 <210> SEQ ID NO: 5

303 <211> LENGTH: 764

304 <212> TYPE: PRT

305 <213> ORGANISM: Beta vulgaris

307 <400> SEQUENCE: 5

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314 20 25 30
317 Val Ser Gln Val Lys Leu Ser Pro Asp Ser Thr Arg Asn Asn Asn Asn
318 35 40 45
321 Lys Asn Gly Phe Ser Asp Ser Leu Ile Glu Glu Glu Glu Gly Leu Asn
322 50 55 60
325 Asn Gln Ser Val Val Ala Lys Cys Ala Glu Ile Gln Asn Ala Ile Ser
326 65 70 75 80
329 Glu Gly Ala Thr Ser Phe Leu Phe Thr Glu Tyr Gln Tyr Val Gly Ile
330 85 90 95
333 Phe Met Val Ala Phe Ala Val Leu Ile Phe Leu Phe Leu Gly Ser Val
334 100 105 110
337 Gln Gly Phe Ser Thr Ser Ser Gln Glu Cys Thr Tyr Asp Lys Thr Arg
338 115 120 125
341 Arg Cys Lys Pro Ala Leu Ala Thr Ala Ile Phe Ser Thr Val Ala Phe
342 130 135 140
345 Leu Leu Gly Ala Ile Thr Ser Leu Gly Ser Gly Phe Phe Gly Met Lys
346 145 150 155 160
349 Ile Ala Thr Tyr Ala Asn Ala Arg Thr Thr Leu Glu Ala Arg Lys Gly
350 165 170 175
353 Val Gly Lys Ala Phe Ile Val Ala Phe Arg Ser Gly Ala Val Met Gly
354 180 185 190
357 Phe Leu Leu Ala Ala Asn Gly Leu Leu Val Leu Tyr Ile Thr Ile Leu
358 195 200 205

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361 Leu Phe Lys Ile Thr Thr Gly Asp Asp Trp Gln Gly Leu Phe Gln Ala
362      210                      215                      220
365 Ile Thr Gly Tyr Gly Leu Gly Gly Ser Ser Met Ala Leu Phe Gly Arg
366 225                      230                      235                      240
369 Val Ala Gly Gly Ile Tyr Thr Lys Ala Ala Asp Val Gly Ala Asp Leu
370                      245                      250                      255
373 Val Gly Lys Val Glu Arg Asp Ile Pro Glu Asp Asp Pro Arg Asn Pro
374                      260                      265                      270
377 Ala Val Ile Ala Asp Asn Val Gly Asp Asn Val Gly Asp Ile Ala Gly
378                      275                      280                      285
381 Met Gly Ser Asp Leu Phe Gly Ser Tyr Ala Glu Ser Ser Cys Ala Ala
382      290                      295                      300
385 Leu Val Val Ala Ser Ile Ser Ser Phe Glu Ile Ser His Asp Leu Thr
386 305                      310                      315                      320
389 Ala Met Met Tyr Pro Leu Leu Val Ser Ser Val Gly Ile Ile Val Cys
390                      325                      330                      335
393 Leu Ile Thr Thr Leu Phe Ala Thr Asp Phe Phe Glu Ile Lys Ala Val
394                      340                      345                      350
397 Lys Glu Ile Glu Pro Ala Leu Lys Lys Gln Leu Ile Ile Ser Thr Ala
398                      355                      360                      365
401 Leu Met Thr Val Gly Val Ala Val Ile Ser Trp Ile Ala Leu Pro Thr
402      370                      375                      380
405 Ser Phe Thr Ile Phe Asp Phe Gly Ser Gln Lys Glu Val Gln Asn Trp
406 385                      390                      395                      400
409 Gln Leu Phe Leu Cys Val Ala Val Gly Leu Trp Ala Gly Leu Ile Ile
410                      405                      410                      415
413 Gly Phe Val Thr Gln Tyr Tyr Thr Ser Asn Ala Tyr Ser Pro Val Gln
414                      420                      425                      430
417 Asp Val Ala Asp Ser Cys Arg Thr Gly Ala Ala Thr Asn Val Ile Phe
418      435                      440                      445
421 Gly Leu Ala Leu Gly Tyr Lys Ser Val Ile Ile Pro Ile Phe Ala Ile
422      450                      455                      460
425 Ala Ile Ser Ile Phe Val Ser Phe Ser Phe Ala Ala Met Tyr Gly Ile
426 465                      470                      475                      480
429 Ala Met Ala Ala Leu Gly Met Leu Ser Thr Ile Ala Thr Gly Leu Ala
430                      485                      490                      495
433 Ile Asp Ala Tyr Gly Pro Ile Ser Asp Asn Ala Gly Gly Ile Ala Glu
434                      500                      505                      510
437 Met Ala Gly Met Ser His Arg Ile Arg Glu Arg Thr Asp Ala Leu Asp
438      515                      520                      525
441 Ala Ala Gly Asn Thr Thr Ala Ala Ile Gly Lys Gly Phe Ala Ile Gly
442      530                      535                      540
445 Ser Ala Ala Leu Val Ser Leu Ala Leu Phe Gly Ala Phe Val Ser Arg
446 545                      550                      555                      560
449 Ala Ser Ile Gln Thr Val Asp Val Leu Thr Pro Lys Val Phe Ile Gly
450                      565                      570                      575
453 Leu Ile Val Gly Ala Met Leu Pro Tyr Trp Phe Ser Ala Met Thr Met
454                      580                      585                      590
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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/549,997

DATE: 10/03/2005

TIME: 14:53:08

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Output Set: N:\CRF4\10032005\J549997.raw

L:14 M:270 C: Current Application Number differs, Replaced Current Application Number

L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date